

Fig. 1

DOCKET NO: 0887-4138PC1

Fig. 2

elk1	---MPVMKGLLAPQNTFLDTIATRFDGTHSNFILANAQVAKGFPIVYCSD	47
erg1	---MPVRRGHVAPQNTFLDTIIRKFEGQSRKFIIANARVEN-CAVIYCND	46
eag1	MTMAGGRRGLVAPQNTFLENIVRRS--NDTNFVLGNAQIVD-WPIVYSND	47
elk1	<u>GFCELAGFARTEVMOKSCSCKFLFGVETNEQLMLQIEKSLEEKVEFKGEI</u>	97
erg1	<u>GFCELCGYSTRAEVMQRPCTCDELHGPRTORRAAQIAQALLGAEEERKVEI</u>	96
eag1	<u>GFCKLSGYHRAEVMOKSSACSFMYGELTDKDTVEKVRQTFENYEMNSFEI</u>	97
elk1	<u>MFYKKNGAPFWCLLDIVPIKNEKGDVVLFLASFKDITDTKVKITSEDKKE</u>	147
erg1	<u>AFYRKDGSCFLCLVDVVPVKNEGDGAVIMFILNFEVMEKDMVGSPAHDNTN</u>	146
eag1	<u>LMYKKNRTPVWFFVKIAPIRNEQDKVVLFLCTFSDITA--FK-QPIKDDS</u>	144
elk1	DRAK-----GRSR-----A	156
erg1	HRGPSTSWLASGRAKTFRLKLPALLALTARESPMRTGSTGSPGAPGAVVV	196
eag1	CKG-----WGKFAR-----	153
elk1	GSHFDSARRRS-----R-----	168
erg1	DVDLTPAAPSS ES LALDEV SAM DNHVAGLGP AE ERRALVGPASASPVASI	246
eag1	---L TR ALTSS-----R-----G-----	163
elk1	-----AVLYHISGHLQ-----	179
erg1	PGPHSPRAQSLNPDASGSSCSLARTRSRESCASVRRASSADDIEAMRAG	296
eag1	-----VLQQLAPSVQ-----	173
elk1	-----	179
erg1	ALPLPPRHASTGAMHPLRSGLLNSTSDSLVRYRTISKIPQITLNFVDLK	346
eag1	-----K	174
elk1	-----RREKNK---LKINNNVFVDKPAFPEYKVSDAK	208
erg1	<u>GDPFLASPTSDREIIAPKIKERTHNVTQVLSLGADVLPYKLOAPR</u>	396
eag1	<u>G-----ENVHKKH---SRLAEVLQLGSDILPQYKQEA</u>	204
-----S1-----		
elk1	KSKFILLHFSTFKAGWDWLILLATFYVAVTVPYNVCFIGNED--LS----	252
erg1	IHRWTILHYSPEKAVWDWLILLVIYTAFTPYSAAFLLKETEDGSQAPD	446
eag1	PPHIIILHYCVFKTTTWDWIIILITFYTAILVPYNVSFKTRQN-N-----	247
-----S2-----		
elk1	---TTRSTTVSDIAVEILFIIDIILNFRTTYVSKSGQVIFEARSICIHVY	299
erg1	CGYACQPLAVVDLLVDIMFIVDILINFRTTYVNANEEVVSHPGRIAVHYF	496
eag1	-----VAWLVVDSIVDVIFLVDIVLNFHTTFVGPAGEVISDPKLIRMYNL	292

DOCKET NO: 0887-4138PC1

Fig. 2 (Cont'd)

	-----S3-----	-----S4-----	
elk1	<u>TTWFIIDLIAALPFDLLYAFNVTVVS---</u>	<u>LVHLLKTVRLLRLLRLLQKLD</u>	346
erg1	<u>KGWFLIDMVAAIPFDLLIFGSGSEE---</u>	<u>LIGLLKTARLLRLVRVARKLD</u>	542
eag1	<u>KTWFVIDLLSCLPYDVINAFENVDEGISS</u>	<u>LFSSLKVVRLRLGRVARKLD</u>	342
	-	-----S5-----	
elk1	<u>RYSQHSTIVLTLLMSMFALLAHWMACIWYVIGKMEREDNSLLKWEVG-WL</u>		395
erg1	<u>RYSEYGA AVLFLMCTFALIAHWLACIWYAIGNMEQPHMDSHIG----</u>	<u>WL</u>	588
eag1	<u>HYIEYGA AVLVLVCVFGLAAHWMACIWYSIGDYEIFDEDTKTIRNNSWL</u>		392
	-----P-----		
elk1	<u>HELGKRLESPYYGNN-----</u>	<u>TLGGPSIRSAYIAALYFTLSSLT SVGF GNV</u>	440
erg1	<u>HNLGDOIGKPYNSSG-----</u>	<u>LGGPSIKDKYVTALYFTFSSLT SVGF GNV</u>	632
eag1	<u>YQLALDIGTPYQFNGSGSGKWE GGP SKNSVYISSLYFTMTSLT SVGF GNI</u>		442
	-----S6-----		
elk1	<u>SANTDAEKIFSICTMLIGALMHALVFGNVTAI IQRMYSRWSLYHTRTKDL</u>		490
erg1	<u>SPNTNSEKIFSICVMLIGSLMYASIFGNVSAI IQRLYSGTARYHTQMLRV</u>		682
eag1	<u>APSTDIEKIFAVAIMMIGSLLYATIFGNVTTFQOMYANTNRYHEMLNSV</u>		492
elk1	<u>KDFIRVHHLPOQLKORMLEYFQTTWSVNNGIDSNELLKDFPDELRS DITM</u>		540
erg1	<u>REFIRFHQIPNPLRQRLEEFQHAWSYTNGIDMNAVLKGFPECLQADICL</u>		732
eag1	<u>RDFLKLYQVPKGLSERVMDYIVSTWSMSRGIDTKKVLOICPKDNRADICV</u>		542
elk1	<u>HLNKEILQLS-LFECASRGCLRSLSLHIKTSFCAPGEYLLRQGDALQAIY</u>		589
erg1	<u>HLNRSLLQHCKPFRGATKGCLRALAMKFKTT HAPPGDTLVHAGDLLTALY</u>		782
eag1	<u>HLNRKV FKEHPAFRLASDGCLRALAMEFQTVHCAPGD LIYHAGEDVDSL C</u>		592
	-----cNBD-----		
elk1	<u>FVCSGSMEVLKDSMVLAILGKGDLIGANLSIKDOVIKTNADV KALTYCDL</u>		639
erg1	<u>FISRGSI EILRGDVVVAILGKN DIFGEPLNLYARPGKSNGDV RALTYCDL</u>		832
eag1	<u>FVVS GSLEVIQDDEVVAILGKG DVF GDVFWKEATLAQSCANVRALTYCDL</u>		642
elk1	<u>QCIILKGLFEVLGLYPEYAHKFVEDIQHDLTYNLREGHESDVISRLSNKS</u>		689
erg1	<u>HKIHRDDLLEVLD MYPEFS DHFWS--SLEITFNLRDTNMIPG-----</u>		872
eag1	<u>HVIKRDALQKVLEFYTAFSHSFSR--NLILT YNLKRIVFR-----</u>		681
elk1	<u>TVPQAEPKNGSIIKKRLPSIVEDEEEEEVEEEEETSLSP IYTRGSSVSHS</u>		739
erg1	<u>-----SPSSAELESGFN RQ-----</u>	<u>RKRKLSFR</u>	894
eag1	<u>-----KISDVKREEEERMK-----</u>	<u>RKNEAPLI</u>	703

DOCKET NO: 0887-4138PC1

Fig. 2 (Cont'd)

elk1	<u>KKTGSSKSYLGLSLKQLTSGTVPFHSP</u> <u>IRVSSANS</u> <u>SPKTKQEADPPNHGTR</u>	789
erg1	<u>RRTDKDTEQPG</u> <u>EV</u> <u>SALG</u> ----- <u>QGP</u> <u>ARVGP</u> <u>GP</u> <u>SCRG</u> - <u>QPGGPWGESP</u> -	935
eag1	<u>LPPDHPVRR</u> <u>LFQR</u> <u>FRQ</u> ----- <u>QKEARLAAE</u> --- <u>RGGRDLDDLDVEK</u> -	741
elk1	<u>KEKNLKVQLCSLGTAGTPELS</u> <u>PRIVDGI</u> <u>EDGNS</u> <u>SEETQT</u> <u>FDGSEQIRPE</u>	839
erg1	----- <u>SSGPSSPES</u> ----- <u>SEDEGPGRSSSPLRLVPF</u>	962
eag1	----- <u>GNALT</u> <u>DHTS</u> ----- <u>ANHSLVKASVVTVRESPA</u>	768
elk1	<u>PRISPSLGESEIGA</u> <u>AF</u> <u>LFIKAEETKQ</u> <u>QINKLN</u> <u>SEVTTLTQ</u> <u>EV</u> <u>SQLGKDMR</u>	889
erg1	<u>S</u> -- <u>SPRPPGD</u> <u>SP</u> <u>GGEPL</u> <u>TEDGEK</u> <u>SSDTCNPL</u> <u>SGAFSGVSN</u> - <u>IFSFWGDSR</u>	1009
eag1	<u>TPVSFQA</u> <u>AST</u> <u>STVSDHAKLHAP</u> - <u>GSECLGP</u> <u>KAGG</u> <u>GDP</u> <u>AKRKGWARFKDAC</u>	817
elk1	<u>SI-MQLLENILSP</u> <u>QOPSQFCSLHPTSICPS</u> <u>RESFQTRVSWSAHQPC</u> <u>LHLQ</u>	938
erg1	<u>GRQYQELPRCPAP</u> ----- <u>APSL</u> <u>LN</u> <u>PLSSPG</u> ----- <u>RRSR</u>	1039
eag1	<u>GK</u> -- <u>GEDWNK</u> <u>VSK</u> ----- <u>AESMETLP</u> <u>PERTKASGEATL</u> <u>KKTD</u>	851
elk1	<u>ANGAHL</u> <u>YHG</u> <u>NVTSDI</u> <u>WSVDPS</u> <u>LVGSNPORTEA</u> <u>HEQSPVDSEL</u> <u>HHSPN</u> <u>LAY</u>	988
erg1	<u>GD</u> ----- <u>VESRLDALQRQDN</u> <u>RL</u> <u>ETRLSAD</u> - <u>MATVLQ</u> <u>LLQ</u> <u>RQMTLVP</u>	1079
eag1	<u>SC</u> ----- <u>DSGITKS</u> <u>DLRLDN</u> <u>VGEAPSPQD</u> - <u>RSPILA</u> <u>EVKHSFYPI</u> <u>P</u>	891
elk1	<u>SPSHCQVIQ</u> <u>EGHLQFLRCISPHSD</u> <u>TTLTPLO</u> <u>SISATLSSSVCS</u> <u>SSETSLH</u>	1038
erg1	<u>PAYSAV</u> <u>TTPG</u> ----- <u>PGPTST</u> <u>SPLL</u> <u>PVGPVPTL</u> <u>TLDSLSQV</u> <u>SQF</u>	1118
eag1	<u>EQT</u> <u>LQATVLE</u> ----- <u>VKHELKEDIKALNAKMTS</u> <u>IEKQLSEILRI</u>	930
elk1	<u>LVLPSRSEEGS</u> <u>ITHGPVSSFS</u> <u>LENLPGSWDREGMMS</u> <u>ASTE</u> <u>PLENFP</u> <u>PVEV</u>	1088
erg1	<u>VAFEEL</u> - <u>PAGAPEL</u> <u>PQDGP</u> <u>TRRLSLPG</u> <u>QLG</u> ----- <u>ALT</u> <u>SQPLHRHGS</u> <u>DPG</u>	1162
eag1	<u>LMSR</u> ----- <u>GSSQSPQD</u> -- <u>ICEVSRP</u> - <u>Q</u> ----- <u>S</u> - <u>PESDRDIFGA</u>	961
elk1	<u>TSTADV</u> <u>KDSKAINV</u>	1102
erg1	<u>S</u> -----	1163
eag1	<u>S</u> -----	962

Key: elk1 (SEQ ID NO:2)
 erg1 (SEQ ID NO:15)
 eag1 (SEQ ID NO:16)

Fig 3

CGGGATCCTT	GTGGACAAAC	TTTGATGGGG	AATTTACACAC	40
AGCGCTGGAA	AAATGCCGGT	TATGAAAGGA	TTGCTGGCGC	80
CACAGAACAC	CTTCCTGGAC	ACTATTGCCA	CCCGTTTCGA	120
CGGAACACAT	AGCAACTTCA	TCCTGGCCAA	TGCCCAAGTG	160
GCAAAAGGTT	TCCCCATAGT	CTACTGTTCA	GATGGCTTCT	200
GTGAGCTGGC	TGGGTTTGCT	CGAACTGAAG	TCATGCAGAA	240
GAGTTGCAGC	TGCAAGTTTC	TGTTTGGGGT	GGAGACCAAC	280
GAGCAGCTGA	TGCTTCAGAT	CGAAAAGTCC	CTGGAGGAGA	320
AGGTAGAGTT	CAAAGGAGAA	ATTATGTTCT	ACAAGAAGAA	360
TGGGGCTCCA	TTTTGGTGCC	TGTTGGATAT	CGTTCCTATA	400
AAGAATGAGA	AAGGAGATGT	GGTCCTTTTC	CTGGCCTCAT	440
TCAAAGATAT	AACAGACACG	AAAGTGAAGA	TTACTTCAGA	480
AGATAAAAAA	GAAGACAGAG	CCAAAGGAAG	ATCAAGAGCA	520
GGGAGCCACT	TCGACTCAGC	CCGCAGACGG	AGCCGAGCAG	560
TCCTTTATCA	CATCTCAGGA	CACCTGCAAA	GAAGAGAAAA	600
GAACAAATTG	AAAATAAATA	ATAACGTGTT	TGTAGATAAA	640
CCGGCGTTTC	CAGAGTATAA	GGTTTCCGAT	GCAAAAAAGT	680
CCAAGTTCAT	CCTGCTGCAC	TTCAGCACTT	TTAAAGCTGG	720
CTGGGACTGG	CTCATTTTGC	TGGCAACGTT	TTATGTTGCT	760
GTGACAGTCC	CTTACAACGT	GTGCTTCATT	GGCAATGAGG	800
ATCTGTCCAC	AACTCGGAGC	ACAACGGTCA	GTGACATCGC	840
TGTGGAGATT	CTCTTCATTA	TAGATATTAT	TCTAAATTTT	880
CGAACAACTT	ATGTCAGCAA	GTCTGGCCAA	GTTATCTTTG	920
AAGCGAGATC	CATTTGCATC	CACTACGTCA	CCACCTGGTT	960
CATCATTGAT	CTGATTGCTG	CCCTGCCCTT	TGACCTCCTG	1000
TATGCTTTCA	ATGTCACAGT	GGTGTCCCTC	GTACATCTTC	1040
TGAAGACTGT	TCGGCTGCTC	CGTCTTTTGC	GCCTCCTGCA	1080
GAAGCTGGAC	CGTTATTCTC	AGCACAGCAC	AATTGTCCTC	1120
ACCCTGCTCA	TGTCCATGTT	TGCTCTCCTT	GCACACTGGA	1160
TGGCATGTAT	CTGGTATGTC	ATTGGAAAAA	TGGAGAGGGA	1200
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GAGCTGGGAA	AGAGACTGGA	ATCTCCGTAC	TACGGCAACA	1280

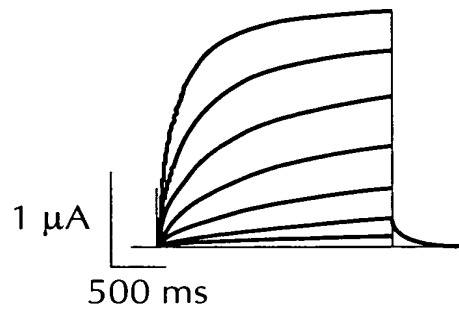
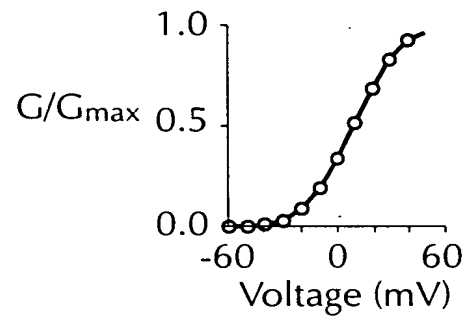
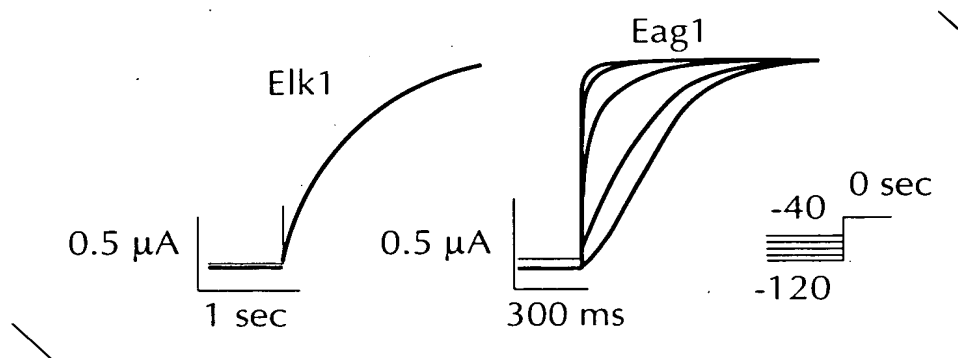
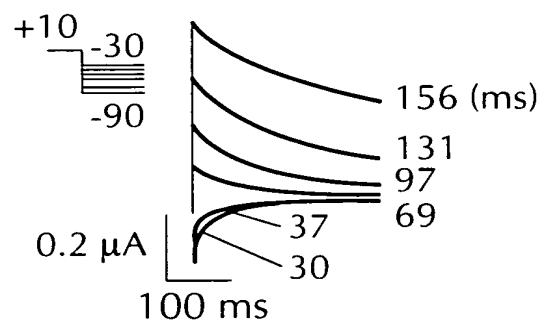
Fig. 3 (Cont'd)

ACACGCTGGG	CGGCCCCGTCC	ATCCGCAGTG	CCTATATCGC	1320
AGCCTTGTAC	TTCACCTCTCA	GCAGCCTCAC	CAGCGTGGGA	1360
TTTGGGAATG	TGTCCGCTAA	CACGGATGCA	GAGAAGATCT	1400
TCTCCATCTG	TACCATGTTG	ATTGGAGCCC	TGATGCATGC	1440
CTTGGTATTT	GGGAATGTGA	CTGCCATCAT	ACAGAGAATG	1480
TACTCTAGAT	GGAGCCTGTA	CCATACTAGA	ACCAAGGACC	1520
TAAAGGACTT	CATCCGTGTG	CATCACCTGC	CCCAGCAACT	1560
CAAGCAGAGG	ATGCTTGAGT	ACTTTCAGAC	AACTTGGTCT	1600
GTCAACAATG	GAATAGATTG	AAATGAGCTT	TTGAAAGACT	1640
TTCCAGATGA	GCTGCGCTCT	GACATCACAA	TGCATCTGAA	1680
CAAGGAGATC	TTACAGCTGT	CCCTGTTTGA	ATGTGCTAGC	1720
CGGGGCTGCC	TCAGGTCTCT	GTCTCTCCAT	ATTAAACCT	1760
CATTCTGTGC	CCCAGGAGAG	TATCTGCTGC	GCCAGGGAGA	1800
TGCGTTGCAG	GCCATCTACT	TCGTGTGCTC	AGGCTCTATG	1840
GAGGTTCTTA	AAGACAGCAT	GGTGTGCTC	ATTCTAGGGA	1880
AGGGGGATTT	AATTGGAGCA	AATTTATCAA	TTAAAGACCA	1920
AGTGATCAAG	ACCAACGCTG	ACGTGAAGGC	TCTGACCTAC	1960
TGTGATCTAC	AGTGCATCAT	CCTGAAAGGT	CTCTTTGAGG	2000
TGCTGGGCCT	TTACCCAGAG	TACGCACACA	AATTCGTAGA	2040
AGACATCCGC	ACGACCTCAC	ATACAACCTT	CGAGAAGGTC	2080
ATGAGAGTGA	TGTAATATCA	AGATTATCGA	ACAAATCTAC	2120
AGTCCCACAG	GCAGAGCCCA	AGGGGAATGG	AAGCATCAAG	2160
AAGAGACTCC	CATCCATTGT	GGAAGATGAG	GAAGAGGAGG	2200
AAGTGAGGGA	AGAGGAGACC	ACCTCCCTTT	CTCCCATCTA	2240
CACAAGGGGA	TCCTCTGTTT	CACACAGCAA	AAAGACTGGA	2280
AGCAGTAAGA	GCTATCTAGG	TTTGAGCTTA	AAGCAACTGA	2320
CCTCAGGAAC	AGTTCCATTG	CACTCACCTA	TCAGAGTCTC	2360
CAGTGCCAAC	TCCCCTAAAA	CCAAGCAGGA	AGCTGACCCA	2400
CCTAACCATG	GCACACGGAA	AGAGAAGAAT	CTGAAAGTTC	2440
AGCTCTGCAG	CCTGGGTACT	GCTGGAACCC	CAGAGCTCAG	2480
TCCGAGGATT	GTCGATGGAA	TTGAAGATGG	CAACAGCAGT	2520
GAGGAAACTC	AGACTTTTGA	TTTTGGCTCT	GAACAAATCA	2560

Fig. 3 (Cont'd)

GGCCAGAGCC	CAGGATTTCC	CCTTCCCTTG	GAGAATCAGA	2600
GATTGGAGCT	GCGTTTCTGT	TCATCAAGGC	TGAAGAAACC	2640
AAGCAGCAGA	TAAACAAGCT	CAACAGTGAG	GTCACAACAT	2680
TGACTCAGGA	GGTCTCCCAG	CTAGGGAAAG	ATATGAGAAG	2720
CATCATGCAA	CTTCTGGAAA	ACATCTTGTC	ACCTCAGCAG	2760
CCATCACAAT	TTTGTTCCT	GCATCCCCT	TCAATCTGTC	2800
CTTCCAGAGA	AAGTTTCCAG	ACTAGGGTGA	GCTGGAGTGC	2840
TCACCAGCCT	TGCCTACACT	TGCAGGCAAA	TGGAGCACAT	2880
CTTTACCATG	GCAATGTAC	CTCTGACATC	TGGAGTGTCT	2920
ACCCCTCCTT	GGTGGGCAGC	AACCCTCAAC	GAAGTGAAGC	2960
TCATGAGCAA	AGTCCAGTAG	ATAGTGAAGT	GCATCATTCT	3000
CCAAACCTGG	CTTATTCCCC	CTCTCACTGC	CAGGTTATCC	3040
AAGAAGGCCA	CTTGCAGTTC	CTAAGGTGCA	TCTCCCCTCA	3080
TTCAGATACC	ACACTGACAC	CTTTGCAGTC	CATCTCAGCC	3120
ACTCTCTCAT	CCTCTGTGTG	CTCCTCATCA	GAAACATCCT	3160
TGCACCTCGT	TCTCCCAAGT	AGGTCAGAGG	AGGGCAGCAT	3200
CACTCATGGA	CCTGTGAGTT	CTTTCAGTTT	GGAAACTTA	3240
CCAGGATCTT	GGGACCGAGA	AGGAATGATG	TCAGCCTCTA	3280
CAGAACCCTT	GGAGAACTTT	CCAGTAGAAG	TTGTCACAAG	3320
CACAGCGGAT	GTAAAAGACA	GCAAAGCCAT	AAACGTATAA	3360
TATCAGCACA	TAAGGGCAGC	TTTCAATGCC	AAATCCACTG	3400
CTGCATGACA	GCTCTAGTTT	GCCTTTGTGG	CTTCTAGCAG	3440
GTGTGGAGCC	TGAGCAAAGT	TAGGAATTCT	GCAGGAAAGA	3480
GGGCAAGGGG	CCAGTAAAAG	GCAGAGCCAC	CTCTATACTG	3520
TAGCAAACAA	TTTCTAGATC	GTAGAAGCAT	AAAACCTTTT	3560
CTGTACAGGT	ATTAACCTTAC	TGGTCTGATT	GACAGACTTT	3600
GGTAACAATC	CTATGACCCA	GAGGGTCTGA	GCAGATAGAA	3640
ACCCAGACA	AAGAGTTTGG	GGATTAGTTT	TGTCATAAGT	3680
GGATTTTTTT	GTGAAGTGCA	GCAAAGGTTT	TTTTTCCTGA	3720
GTGCCTGGTT	GTCATTCCTG	AA		3922

8/11

FIG. 4A**FIG. 4B****FIG. 4C****FIG. 4D**

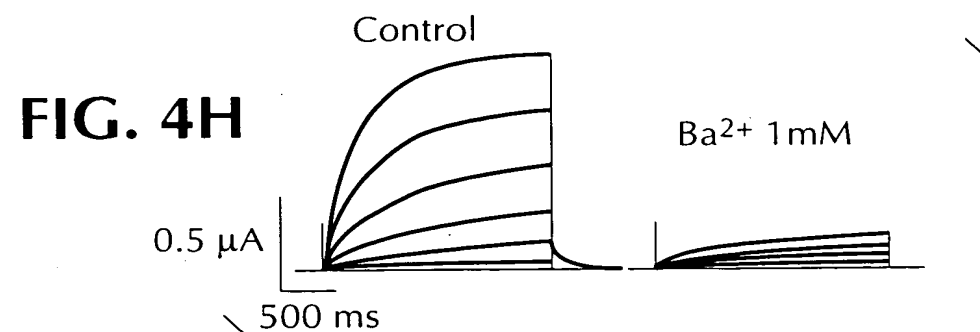
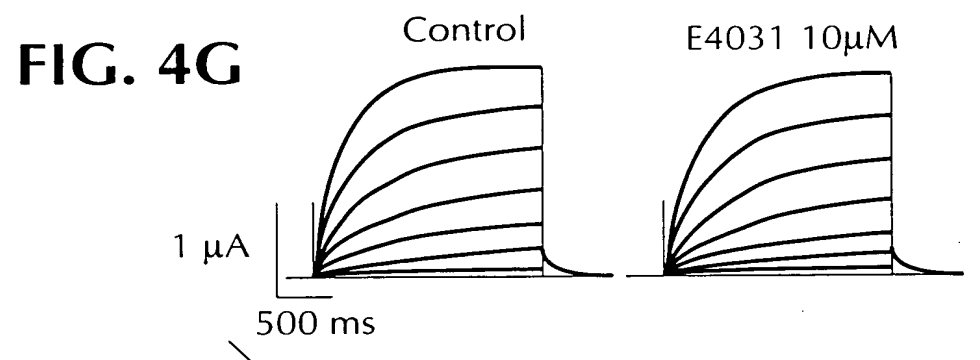
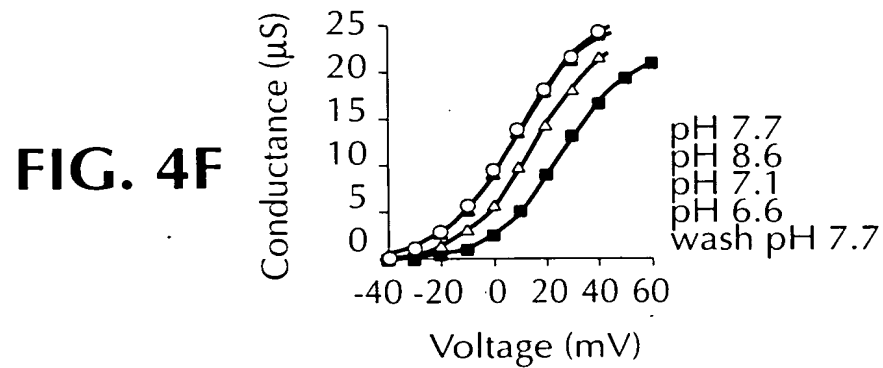
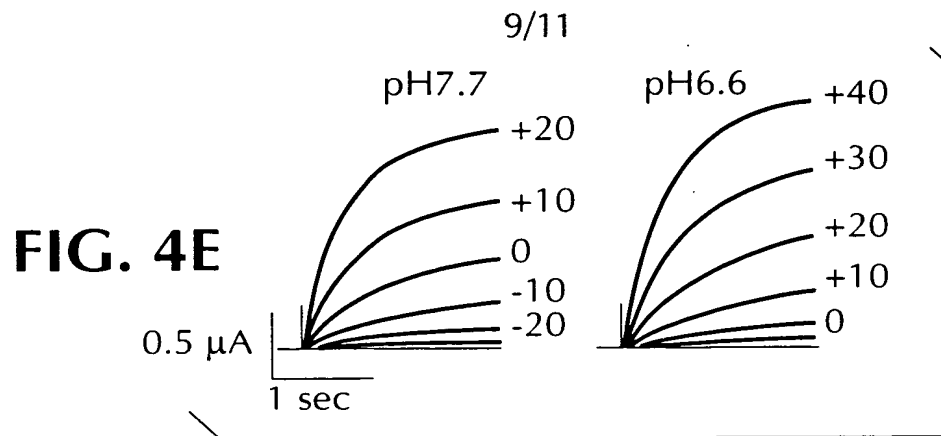


FIG. 5A

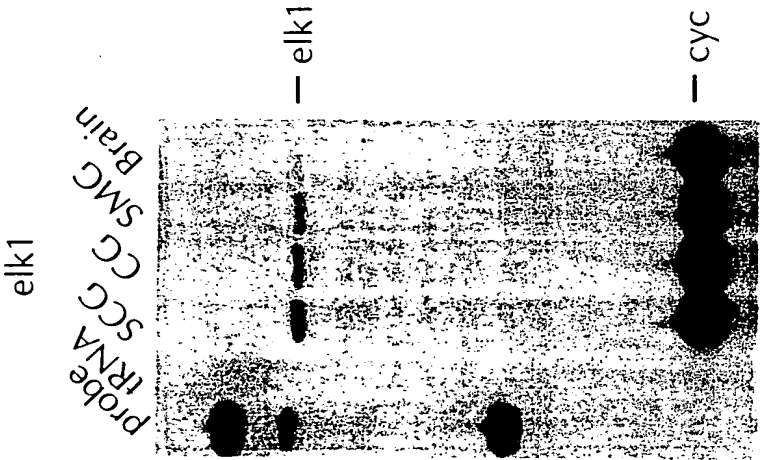


FIG. 5B

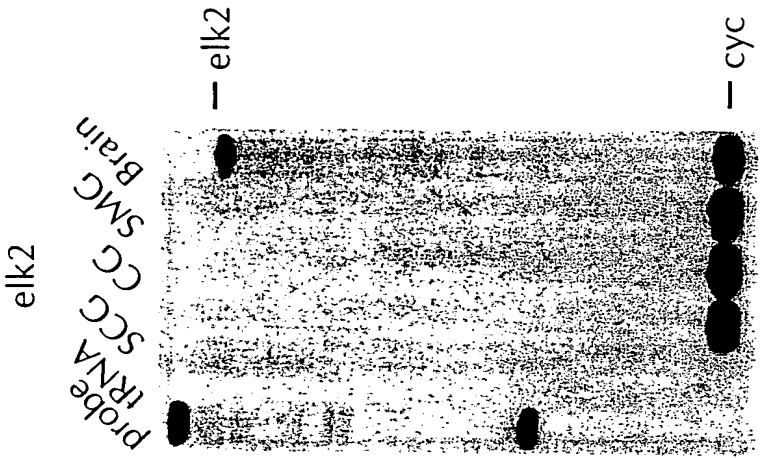
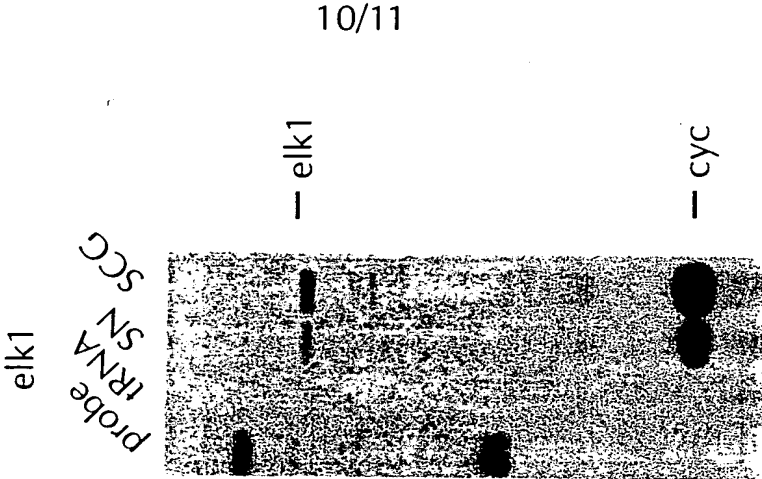


FIG. 5C



11/11

FIG. 5D

FIG. 5E

FIG. 5F

